

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/591,633
Source: IFWP
Date Processed by STIC: 9/18/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/591,633

CRF Edit Date: 9/18/06
Edited by: RZ

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

___ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

✓ Other: Sequence 1 - corrected <2227 response

Revised 09/09/2003



IFWP

RAW SEQUENCE LISTING

DATE: 09/18/2006

PATENT APPLICATION: US/10/591,633

TIME: 16:31:09

Input Set : N:\AMC\3696-029-Sequence Listing.txt

Output Set: N:\CRF4\09182006\J591633.raw

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3 <110> APPLICANT: SIRS-Lab GmbH
5 <120> TITLE OF INVENTION: Method of enriching/separating prokaryotic DNA by means of
6     a protein which specifically binds DNA containing non-methylated
7     CpG motifs
9 <130> FILE REFERENCE: Pat 3696/29-PCT
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/591,633
C--> 12 <141> CURRENT FILING DATE: 2006-09-05
14 <160> NUMBER OF SEQ ID NOS: 8
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 543
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(543)
27 <400> SEQUENCE: 1
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29 Gly Gly Gly Arg Lys Arg Pro Val Pro Asp Pro Asn Leu Gln Arg Arg
30   1               5               10               15
32 gca ggg tca ggg aca ggg gtt ggg gcc atg ctt gct cgg ggc tct gct      96
33 Ala Gly Ser Gly Thr Gly Val Gly Ala Met Leu Ala Arg Gly Ser Ala
34   20               25               30
36 tcg ccc cac aaa tcc tct ccg cag ccc ttg gtg gcc aca ccc agc cag     144
37 Ser Pro His Lys Ser Ser Pro Gln Pro Leu Val Ala Thr Pro Ser Gln
38   35               40               45
40 cat cac cag cag cag cag cag cag atc aaa cgg tca gcc cgc atg tgt     192
41 His His Gln Gln Gln Gln Gln Gln Ile Lys Arg Ser Ala Arg Met Cys
42   50               55               60
44 ggt gag tgt gag gca tgt cgg cgc act gag gac tgt ggt cac tgt gat     240
45 Gly Glu Cys Glu Ala Cys Arg Arg Thr Glu Asp Cys Gly His Cys Asp
46  65               70               75               80
48 ttc tgt cgg gac atg aag aag ttc ggg ggc ccc aac aag atc cgg cag     288
49 Phe Cys Arg Asp Met Lys Lys Phe Gly Gly Pro Asn Lys Ile Arg Gln
50   85               90               95
52 aag tgc cgg ctg cgc cag tgc cag ctg cgg gcc cgg gaa tcg tac aag     336
53 Lys Cys Arg Leu Arg Gln Cys Gln Leu Arg Ala Arg Glu Ser Tyr Lys
54  100              105              110
56 tac ttc cct tcc tcg ctc tca cca gtg acg ccc tca gag tcc ctg cca     384
57 Tyr Phe Pro Ser Ser Leu Ser Pro Val Thr Pro Ser Glu Ser Leu Pro
58  115              120              125
60 agg ccc cgc cgg cca ctg ccc acc caa cag cag cca cag cca tca cag     432
61 Arg Pro Arg Arg Pro Leu Pro Thr Gln Gln Gln Pro Gln Pro Ser Gln

```

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Output Set: N:\CRF4\09182006\J591633.raw

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62      130      135      140
64 aag tta ggg cgc atc cgt gaa gat gag ggg gca gtg gcg tca tca aca 480
65 Lys Leu Gly Arg Ile Arg Glu Asp Glu Gly Ala Val Ala Ser Ser Thr
66 145      150      155      160
68 gtc aag gag cct cct gag gct aca gcc aca cct gag cca ctc tca gat 528
69 Val Lys Glu Pro Pro Glu Ala Thr Ala Thr Pro Glu Pro Leu Ser Asp
70      165      170      175
72 gag gac cta cct ctg 543
73 Glu Asp Leu Pro Leu
74      180
77 <210> SEQ ID NO: 2
78 <211> LENGTH: 181
79 <212> TYPE: PRT
80 <213> ORGANISM: Homo sapiens
82 <400> SEQUENCE: 2
83 Gly Gly Gly Arg Lys Arg Pro Val Pro Asp Pro Asn Leu Gln Arg Arg
84 1 5 10 15
86 Ala Gly Ser Gly Thr Gly Val Gly Ala Met Leu Ala Arg Gly Ser Ala
87 20 25 30
89 Ser Pro His Lys Ser Ser Pro Gln Pro Leu Val Ala Thr Pro Ser Gln
90 35 40 45
92 His His Gln Gln Gln Gln Gln Gln Ile Lys Arg Ser Ala Arg Met Cys
93 50 55 60
95 Gly Glu Cys Glu Ala Cys Arg Arg Thr Glu Asp Cys Gly His Cys Asp
96 65 70 75 80
98 Phe Cys Arg Asp Met Lys Lys Phe Gly Gly Pro Asn Lys Ile Arg Gln
99 85 90 95
101 Lys Cys Arg Leu Arg Gln Cys Gln Leu Arg Ala Arg Glu Ser Tyr Lys
102 100 105 110
104 Tyr Phe Pro Ser Ser Leu Ser Pro Val Thr Pro Ser Glu Ser Leu Pro
105 115 120 125
107 Arg Pro Arg Arg Pro Leu Pro Thr Gln Gln Gln Pro Gln Pro Ser Gln
108 130 135 140
110 Lys Leu Gly Arg Ile Arg Glu Asp Glu Gly Ala Val Ala Ser Ser Thr
111 145 150 155 160
113 Val Lys Glu Pro Pro Glu Ala Thr Ala Thr Pro Glu Pro Leu Ser Asp
114 165 170 175
116 Glu Asp Leu Pro Leu
117 180
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 28
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial sequence
126 <220> FEATURE:
127 <223> OTHER INFORMATION: Description of artificial sequence: Primer
129 <400> SEQUENCE: 3
130 ggatccggtg gagggcgcaa gaggcctg 28
133 <210> SEQ ID NO: 4
134 <211> LENGTH: 27

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RAW SEQUENCE LISTING

DATE: 09/18/2006

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TIME: 16:31:09

Input Set : N:\AMC\3696-029-Sequence Listing.txt

Output Set: N:\CRF4\09182006\J591633.raw

135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial sequence
138 <220> FEATURE:
139 <223> OTHER INFORMATION: Description of artificial sequence: Primer
141 <400> SEQUENCE: 4
142 aagcttagag gtaggtcctc atctgag 27
145 <210> SEQ ID NO: 5
146 <211> LENGTH: 26
147 <212> TYPE: DNA
148 <213> ORGANISM: Artificial sequence
150 <220> FEATURE:
151 <223> OTHER INFORMATION: Description of artificial sequence: Primer
153 <400> SEQUENCE: 5
154 agcatacaag caaatTTTTT acaccg 26
157 <210> SEQ ID NO: 6
158 <211> LENGTH: 24
159 <212> TYPE: DNA
160 <213> ORGANISM: Artificial sequence
162 <220> FEATURE:
163 <223> OTHER INFORMATION: Description of artificial sequence: Primer
165 <400> SEQUENCE: 6
166 gttctgttat tgacacccgc aatt 24
169 <210> SEQ ID NO: 7
170 <211> LENGTH: 24
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: Description of artificial sequence: Primer
177 <400> SEQUENCE: 7
178 ccttcctaataatcctgcgcg atgt 24
181 <210> SEQ ID NO: 8
182 <211> LENGTH: 28
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Description of artificial sequence: Primer
189 <400> SEQUENCE: 8
190 ctgaaggtag cattagtctt tgataacg 28

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/591,633

DATE: 09/18/2006

TIME: 16:31:10

Input Set : N:\AMC\3696-029-Sequence Listing.txt

Output Set: N:\CRF4\09182006\J591633.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

**Raw Sequence Listing before editing
(for reference only)**



IFWP

RAW SEQUENCE LISTING

DATE: 09/15/2006

PATENT APPLICATION: US/10/591,633

TIME: 09:35:15

Input Set : F:\3696-029-Sequence Listing.txt

Output Set: N:\CRF4\09152006\J591633.raw

3 <110> APPLICANT: SIRS-Lab GmbH
 5 <120> TITLE OF INVENTION: Method of enriching/separating prokaryotic DNA by means of
 6 a protein which specifically binds DNA containing non-methylated
 7 CpG motifs
 9 <130> FILE REFERENCE: Pat 3696/29-PCT
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 19 <211> LENGTH: 543
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Homo sapiens
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 W--> 25 <222> LOCATION: (1)..(561) (543)
 27 <400> SEQUENCE: 1

| | | |
|----|-----------------------------------------------------------------|-----|
| 28 | ggt gga ggg cgc aag agg cct gtc cct gat cca aac ctg cag cgc cgg | 48 |
| 29 | Gly Gly Gly Arg Lys Arg Pro Val Pro Asp Pro Asn Leu Gln Arg Arg | |
| 30 | 1 5 10 15 | |
| 32 | gca ggg tca ggg aca ggg gtt ggg gcc atg ctt gct cgg ggc tct gct | 96 |
| 33 | Ala Gly Ser Gly Thr Gly Val Gly Ala Met Leu Ala Arg Gly Ser Ala | |
| 34 | 20 25 30 | |
| 36 | tcg ccc cac aaa tcc tct ccg cag ccc ttg gtg gcc aca ccc agc cag | 144 |
| 37 | Ser Pro His Lys Ser Ser Pro Gln Pro Leu Val Ala Thr Pro Ser Gln | |
| 38 | 35 40 45 | |
| 40 | cat cac cag cag cag cag cag cag atc aaa cgg tca gcc cgc atg tgt | 192 |
| 41 | His His Gln Gln Gln Gln Gln Gln Ile Lys Arg Ser Ala Arg Met Cys | |
| 42 | 50 55 60 | |
| 44 | ggt gag tgt gag gca tgt cgg cgc act gag gac tgt ggt cac tgt gat | 240 |
| 45 | Gly Glu Cys Glu Ala Cys Arg Arg Thr Glu Asp Cys Gly His Cys Asp | |
| 46 | 65 70 75 80 | |
| 48 | ttc tgt cgg gac atg aag aag ttc ggg ggc ccc aac aag atc cgg cag | 288 |
| 49 | Phe Cys Arg Asp Met Lys Lys Phe Gly Gly Pro Asn Lys Ile Arg Gln | |
| 50 | 85 90 95 | |
| 52 | aag tgc cgg ctg cgc cag tgc cag ctg cgg gcc cgg gaa tcg tac aag | 336 |
| 53 | Lys Cys Arg Leu Arg Gln Cys Gln Leu Arg Ala Arg Glu Ser Tyr Lys | |
| 54 | 100 105 110 | |
| 56 | tac ttc cct tcc tcg ctc tca cca gtg acg ccc tca gag tcc ctg cca | 384 |
| 57 | Tyr Phe Pro Ser Ser Leu Ser Pro Val Thr Pro Ser Glu Ser Leu Pro | |
| 58 | 115 120 125 | |
| 60 | agg ccc cgc cgg cca ctg ccc acc caa cag cag cca cag cca tca cag | 432 |
| 61 | Arg Pro Arg Arg Pro Leu Pro Thr Gln Gln Gln Pro Gln Pro Ser Gln | |

**Does Not Comply
Corrected Diskette Needed**

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65 Lys Leu Gly Arg Ile Arg Glu Asp Glu Gly Ala Val Ala Ser Ser Thr
66 145      150      155      160
68 gtc aag gag cct cct gag gct aca gcc aca cct gag cca ctc tca gat 528
69 Val Lys Glu Pro Pro Glu Ala Thr Ala Thr Pro Glu Pro Leu Ser Asp
70      165      170      175
72 gag gac cta cct ctg 543
73 Glu Asp Leu Pro Leu
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82 <400> SEQUENCE: 2
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84 1 5 10 15
86 Ala Gly Ser Gly Thr Gly Val Gly Ala Met Leu Ala Arg Gly Ser Ala
87 20 25 30
89 Ser Pro His Lys Ser Ser Pro Gln Pro Leu Val Ala Thr Pro Ser Gln
90 35 40 45
92 His His Gln Gln Gln Gln Gln Ile Lys Arg Ser Ala Arg Met Cys
93 50 55 60
95 Gly Glu Cys Glu Ala Cys Arg Arg Thr Glu Asp Cys Gly His Cys Asp
96 65 70 75 80
98 Phe Cys Arg Asp Met Lys Lys Phe Gly Gly Pro Asn Lys Ile Arg Gln
99 85 90 95
101 Lys Cys Arg Leu Arg Gln Cys Gln Leu Arg Ala Arg Glu Ser Tyr Lys
102 100 105 110
104 Tyr Phe Pro Ser Ser Leu Ser Pro Val Thr Pro Ser Glu Ser Leu Pro
105 115 120 125
107 Arg Pro Arg Arg Pro Leu Pro Thr Gln Gln Gln Pro Gln Pro Ser Gln
108 130 135 140
110 Lys Leu Gly Arg Ile Arg Glu Asp Glu Gly Ala Val Ala Ser Ser Thr
111 145 150 155 160
113 Val Lys Glu Pro Pro Glu Ala Thr Ala Thr Pro Glu Pro Leu Ser Asp
114 165 170 175
116 Glu Asp Leu Pro Leu
117 180
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 28
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial sequence
126 <220> FEATURE:
127 <223> OTHER INFORMATION: Description of artificial sequence: Primer
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DATE: 09/15/2006

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Input Set : F:\3696-029-Sequence Listing.txt

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139 <223> OTHER INFORMATION: Description of artificial sequence: Primer
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145 <210> SEQ ID NO: 5
146 <211> LENGTH: 26
147 <212> TYPE: DNA
148 <213> ORGANISM: Artificial sequence
150 <220> FEATURE:
151 <223> OTHER INFORMATION: Description of artificial sequence: Primer
153 <400> SEQUENCE: 5
154 agcatacaag caaatTTTTT acaccg 26
157 <210> SEQ ID NO: 6
158 <211> LENGTH: 24
159 <212> TYPE: DNA
160 <213> ORGANISM: Artificial sequence
162 <220> FEATURE:
163 <223> OTHER INFORMATION: Description of artificial sequence: Primer
165 <400> SEQUENCE: 6
166 gttctgttat tgacaccgc aatt 24
169 <210> SEQ ID NO: 7
170 <211> LENGTH: 24
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: Description of artificial sequence: Primer
177 <400> SEQUENCE: 7
178 ccttcctaataat aatcctgcgg atgt 24
181 <210> SEQ ID NO: 8
182 <211> LENGTH: 28
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Description of artificial sequence: Primer
189 <400> SEQUENCE: 8
190 ctgaaggtag cattagtctt tgataacg 28

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/591,633

DATE: 09/15/2006

TIME: 09:35:16

Input Set : F:\3696-029-Sequence Listing.txt

Output Set: N:\CRF4\09152006\J591633.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:25 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:1, CDS LOCATION: (1)..(561)